

Official, please enter.

Malicka

20

25

30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
35 40

<210> 32
<211> 262
<212> DNA
<213> Homo sapiens

<220>
<223> Intron X. Complete length unknown

<400> 32
gacagtcacc agggggggttg accgccggac tgggcgtccc cagggttgac tataggacca 60
ggtgtccagg tgccttgcga gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
cgtggccccc ggcattggcct tctgcgtgtg ctgccgtggg tgccttgagc cctcactgag 180
tcggtggggg cttgtggcct cccgtgagct tccccctagt ctggtgtctg gctgagcaag 240
cctcctgagg ggctctctat tg 262

<210> 33
<211> 218
<212> DNA
<213> Homo sapiens

<220>
<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33
gtggctgtgc tttggtttaa cttccttttt aaccagaagt gogtttgagc cccacatttg 60
gtatcagctt agatgaaggg cccggaggag gggccacggg acacagccag ggccatggca 120
cggcgccccc ccatttgtgc gcacagttag gtggccgagg tgccggtgcc tccagaaaaa 180
cagcgtgggg gtgtaggggg agctcctggg gcaggagac 218

<210> 34
<211> 2031
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1767)..(1769)
<223> Wherein N is A, C, G or T

<220>
<223> Truncated Telomerase

<400> 34
atgcgcgcgc ctcctccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgag 120
cgcggggacc cggcggtttt ccgcgcgtg gtggccagc gcctgggtgt cgtgcctctg 180
gacgcacggc cgccccccgc cgccccctcc ttccgcagg tgtcctgctt gaaggagctg 240
gtggcccgag tgcctgagag gctgtgcgag cgcggcgcga agaactgctt ggccttcggc 300
ttcgcgctgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360
agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgct ggggctgctg 420
ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cagcgtgcgc gctctttgtg 480

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
 1045 1050 1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
 1060 1065 1070

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1075 1080

<210> 51
 <211> 2135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified base
 <222> (1871)..(1873)
 <223> Wherein N is A, C, G or T

<220>
 <223> Truncated Telomerase (ver. 2); with
 Intron Y

<400> 51
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgcccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180
 gacgcacggc cccccccgc cccccctcc ttccgccagg tgggctccc cgggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtcgc 360
 agaggctgtg cgcgcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggccgcggg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccacaa 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtggggc 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctgggtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgtgtccact caggccccgc 660
 ccccgccaca cgctagtggg ccccgaaagg gtctgggatg cgaacggggc tgggaaccata 720
 gcgtcagggg ggcgggggtc cccctggggc tgccagcccc ggggtgcgagg aggcgcgggg 780
 gcagtgcag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gccctgagc 840
 cggagcggac gcccggttgg cagggtcctt gggccacccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgcactccc acccatcctt gggccgcccag caccacgcgg 1020
 gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgtcggag gctcgtggag accatcttcc 1200
 tgggttccag gccctggatg ccagggaact cccgcaggtt gccccgctg cccagcgct 1260
 actggcaaat gcggccctg tttctggagc tgcttgggaa ccacgcgcag tgccccacg 1320
 ggggtgctct caagacgcac tgcccgctgc gagctgcggt caccacagca gccgggtgtc 1380
 gtgcccggga gaagcccag ggctctgtgg cggccccga ggaggaggac acagacccc 1440
 gtgcctggt gcagctgtc cgcacgcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct gcgcggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttctcag gaacaccaag aagttcatct ccctggggaa gcattgccaag ctctcgtcgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcacgtc tgctgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtgcgcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtotggagc aagttgcaaa 1860
 gcattggaat nnnagacgtc accagggggg ttgaccgccc gactgggcgt cccaggggtt 1920

gactatagga ccagggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
 tggcatgggt ggacgtggcc ccgggcatgg ccttctgcgt gtgctgccgt gggtgccctg 2040
 agccctcact gagtcgggtgg gggcttgtgg ctcccggtga gcttccccct agtctgttgt 2100
 ctggctgagc aagcctcctg aggggctctc tattg 2135

<210> 52
 <211> 622
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Telomerase (ver.2); encoded
 by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser

```

225                230                235                240
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
                245                250                255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
                260                265                270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
                275                280                285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
                290                295                300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305                310                315                320
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
                325                330                335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
                340                345                350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
                355                360                365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu      370
375                380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385                390                395                400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
                405                410                415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
                420                425                430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
                435                440                445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
                450                455                460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465                470                475                480
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
                485                490                495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
                500                505                510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
                515                520                525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
                530                535                540

```

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
610 615 620

<210> 53

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<223> Splicing Variant of Human Telomerase encoded by
Intron Y, ORF2, before the termination codon.

SEQ ID NOS: 51,55,59,63,67,71,75,79,83 encode this
fragment

<400> 53

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala
65 70 75 80

Ser Gly Trp Gly

<210> 54

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Telomerase (ver. 2); encoded
by SEQ ID NO:51, with Y intron, ORF2, after the
termination codon

<210> 154
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 154
 Arg Ala Thr Ser
 1

<210> 155
 <211> 622
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Telomerase (ver.2); encoded
 by SEQ ID NO:51, with Y Intron ORF3

<400> 155
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro